

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 172.793 Seconds  
(without alignments)  
809.667 Million cell updates/sec

Title: US-10-053-975A-1  
Perfect score: 2047  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSDLY 390

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2047	100.0	390	2	AAW93424	Aaw93424 Human NHT
2	2047	100.0	390	5	ABP52191	Abp52191 Human tum
3	2047	100.0	390	6	ABG73787	Abg73787 Human tum
4	2047	100.0	390	7	ADC35176	Adc35176 Novel hum
5	2047	100.0	390	8	ADF91425	Adf91425 TSG101 #S
6	2047	100.0	390	8	ADL82957	Adl82957 Human PRO
7	2047	100.0	390	8	ADN12256	Adn12256 Human TSG
8	2047	100.0	390	8	ADO43235	Ado43235 Human TSG
9	2047	100.0	390	8	ADO43233	Ado43233 Human TSG

10	2047	100.0	390	8	ADP82614	Adp82614	Human	tum
11	2042	99.8	390	6	AAE34885	Aae34885	Human	Tsg
12	2002	97.8	380	2	AAW19111	Aaw19111	Human	tum
13	1945.5	95.0	391	6	AAE34884	Aae34884	Mouse	Tsg
14	1945.5	95.0	391	7	ADB85228	Adb85228	Mouse	tum
15	1900.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum
16	1900.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg
17	1900.5	92.8	381	6	ABG73788	Abg73788	Murine	ts
18	1900.5	92.8	381	7	ADC35178	Adc35178	Human	tsg
19	1404	68.6	307	5	ABP41729	Abp41729	Human	ova
20	1162	56.8	237	4	AAE09328	Aae09328	Human	int
21	809.5	39.5	331	4	ABB64607	Abb64607	Drosophil	
22	776	37.9	145	8	ADF91424	Adf91424	TSG101UEV	
23	479	23.4	90	3	AAG01689	Aag01689	Human	sec
24	455	22.2	398	3	AAG06370	Aag06370	Arabidops	
25	455	22.2	398	8	ADN73283	Adn73283	Thale	cre
26	455	22.2	412	3	AAG06369	Aag06369	Arabidops	
27	435	21.3	379	5	ABP43551	Abp43551	L-lactate	
28	435	21.3	379	8	ADH13697	Adh13697	Human	ENZ
29	424	20.7	340	3	AAG06371	Aag06371	Arabidops	
30	390	19.1	87	8	ABO55273	Abo55273	Human	gen
31	380	18.6	322	3	AAG13898	Aag13898	Arabidops	
32	371	18.1	341	4	AAB93473	Aab93473	Human	pro
33	371	18.1	433	7	ADM29340	Adm29340	Human	nov
34	346	16.9	146	3	AAB53717	Aab53717	Human	col
35	339	16.6	452	4	AAU23116	Aau23116	Novel	hum
36	328	16.0	73	8	ABO55495	Abo55495	Human	gen
37	267.5	13.1	288	3	AAG13899	Aag13899	Arabidops	
38	161.5	7.9	168	3	AAG13900	Aag13900	Arabidops	
39	161	7.9	485	3	AAB57086	Aab57086	Human	pro
40	160	7.8	466	6	ABO07215	Abo07215	Human	p53
41	160	7.8	466	7	ADD47589	Add47589	Human	Pro
42	160	7.8	466	7	ADI15879	Adi15879	Human	PP
43	160	7.8	466	7	ADJ68571	Adj68571	Human	hea
44	153	7.5	218	4	ABG18833	Abg18833	Novel	hum
45	151	7.4	466	2	AAR07084	Aar07084	Recombina	

# ALIGNMENTS

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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 35.897 Seconds  
(without alignments)  
1045.338 Million cell updates/sec

Title: US-10-053-975A-1  
Perfect score: 2047  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSDLY 390

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	658	32.1	404	2	H88650		protein C09G12.9 [
2	388	19.0	83	2	I48283		gene CC2 protein -
3	153.5	7.5	169	2	T34520		hypothetical prote
4	148.5	7.3	397	2	JC8036		hepatocellular car
5	147	7.2	488	1	LUHU7		annexin VII, long
6	145.5	7.1	212	2	S74288		hypothetical prote
7	142	6.9	505	2	A53152		annexin XI - human
8	141	6.9	463	2	S29170		annexin VII - mous
9	138.5	6.8	827	2	T39608		zinc finger transc
10	136.5	6.7	503	1	LURB11		annexin XI - rabbi
11	135.5	6.6	437	2	T14192		extensin homolog T
12	134	6.5	198	2	D70509		hypothetical prote
13	134	6.5	485	2	T37550		hypothetical coile

14	132.5	6.5	671	2	T36037	probable export as
15	131.5	6.4	370	2	T42532	hypothetical prote
16	131	6.4	1613	2	S39059	protein BRG1 - hum
17	131	6.4	1880	2	T18531	tractin - medicina
18	130.5	6.4	338	2	I53043	transforming prote
19	130	6.4	1647	2	S45252	SNF2beta protein -
20	128.5	6.3	1006	2	T42731	atrophin-1 related
21	128	6.3	139	2	H84809	hypothetical prote
22	128	6.3	3942	2	T42730	Bassoon protein -
23	127	6.2	1184	2	G01763	atrophin-1 - human
24	126.5	6.2	678	2	H88187	protein C18H9.8 [i
25	126	6.2	1453	2	S21626	collagen alpha 1(I
26	125	6.1	2715	2	T13049	eyelid - fruit fly
27	124.5	6.1	669	2	T28754	hypothetical prote
28	124.5	6.1	990	2	T14756	hypothetical prote
29	124	6.1	964	2	T21865	hypothetical prote
30	123.5	6.0	279	2	T05421	hypothetical prote
31	123.5	6.0	380	2	S51797	vasodilator-stimul
32	123	6.0	564	2	H70804	hypothetical prote
33	122	6.0	887	1	S57219	1-phosphatidylinos
34	122	6.0	978	2	A70387	conserved hypothet
35	122	6.0	1181	2	C86349	F8K7.4 protein - A
36	121.5	5.9	551	2	S57447	HPBR11-7 protein -
37	121	5.9	792	2	T49989	hypothetical prote
38	120.5	5.9	1902	2	C97702	cell surface antig
39	119.5	5.8	503	1	LUBO11	annexin XI form A
40	119.5	5.8	505	1	S23447	annexin XI form B
41	119	5.8	577	2	T09024	proline-rich prote
42	119	5.8	859	2	H70327	DNA mismatch repai
43	119	5.8	1357	2	T29265	hypothetical prote
44	119	5.8	1422	2	T24212	hypothetical prote
45	118.5	5.8	384	2	S51796	vasodilator-stimul

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 188.612 Seconds  
(without alignments)  
1189.726 Million cell updates/sec

Title: US-10-053-975A-1  
Perfect score: 2047  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....FQLRALMQKARKTAGLSPLY 390

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2047	100.0	390	1 T101_HUMAN	Q99816 homo sapien
2	2041	99.7	390	2 Q9BUM5	Q9bum5 homo sapien
3	1945.5	95.0	391	1 T101_MOUSE	Q61187 mus musculu
4	1927.5	94.2	391	2 Q6IRE4	Q6ire4 rattus norv
5	1927.5	94.2	391	2 AAH70951	Aah70951 rattus no
6	1908.5	93.2	391	2 Q7TSE5	Q7tse5 rattus norv
7	1899	92.8	392	2 Q9I8G8	Q9i8g8 chelonia my
8	1705.5	83.3	390	2 Q6IQ70	Q6iq70 brachydanio
9	1705.5	83.3	390	2 AAH71540	Aah71540 brachydan
10	1685	82.3	394	2 Q6NUD5	Q6nud5 xenopus lae
11	1685	82.3	394	2 AAH68660	Aah68660 xenopus l
12	1682.5	82.2	395	2 Q6P2Z8	Q6p2z8 xenopus tro
13	1682.5	82.2	395	2 AAH64236	Aah64236 xenopus t
14	1024.5	50.0	408	2 Q9VVA7	Q9vva7 drosophila
15	976	47.7	402	2 Q7Q6B6	Q7q6b6 anopheles g

16	754.5	36.9	425	2	O76258	O76258	caenorhabdi
17	749.5	36.6	326	2	Q6DDX9	Q6ddx9	xenopus lae
18	599	29.3	249	2	Q8MQZ0	Q8mqz0	drosophila
19	522	25.5	114	2	Q7T2M2	Q7t2m2	ameiurus ne
20	455	22.2	398	2	Q9LHG8	Q9lhg8	arabidopsis
21	435	21.3	379	2	Q8IX04	Q8ix04	homo sapien
22	432	21.1	580	2	Q7S4R9	Q7s4r9	neurospora
23	429.5	21.0	249	2	Q7TQD3	Q7tqd3	mus musculu
24	427	20.9	174	2	O08761	O08761	mus musculu
25	398	19.4	471	2	Q6DBY5	Q6dby5	brachydanio
26	396.5	19.4	402	2	Q6ESB7	Q6esb7	oryza sativ
27	391	19.1	368	2	Q9FFY6	Q9fffy6	arabidopsis
28	388	19.0	83	2	Q6LBE4	Q6lbe4	mus musculu
29	388	19.0	83	2	CAA57762	Caa57762	mus muscu
30	371	18.1	177	2	Q96FF5	Q96ff5	homo sapien
31	371	18.1	341	2	Q9NUX7	Q9nux7	homo sapien
32	341	16.7	357	2	Q6P2F0	Q6p2f0	homo sapien
33	341	16.7	357	2	AAH64566	Aah64566	homo sapi
34	303	14.8	385	1	ST22_YEAST	P25604	saccharomyc
35	301.5	14.7	378	2	Q873M7	Q873m7	yarrowia li
36	301.5	14.7	378	2	Q6C148	Q6c148	yarrowia li
37	294	14.4	111	2	Q8BU96	Q8bu96	mus musculu
38	294	14.4	468	2	Q6FS29	Q6fs29	candida gla
39	239	11.7	496	2	Q6BID5	Q6bid5	debaryomyce
40	215	10.5	445	2	Q75EU1	Q75eu1	ashbya goss
41	215	10.5	445	2	AAS50360	Aas50360	ashbya go
42	169	8.3	376	2	P78998	P78998	saccharomyc
43	160	7.8	466	1	ANX7_HUMAN	P20073	homo sapien
44	160	7.8	466	2	BAB93492	Bab93492	homo sapi
45	160	7.8	466	2	AAP35851	Aap35851	homo sapi

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 62.0281 Seconds  
(without alignments)  
809.667 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_1\_140  
Perfect score: 750  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	750	100.0	145	8	ADF91424	Adf91424 TSG101UEV
2	750	100.0	237	4	AAE09328	Aae09328 Human int
3	750	100.0	390	2	AAW93424	Aaw93424 Human NHT
4	750	100.0	390	5	ABP52191	Abp52191 Human tum
5	750	100.0	390	6	AAE34885	Aae34885 Human Tsg
6	750	100.0	390	6	ABG73787	Abg73787 Human tum
7	750	100.0	390	7	ADC35176	Adc35176 Novel hum
8	750	100.0	390	8	ADF91425	Adf91425 TSG101 #S
9	750	100.0	390	8	ADL82957	Adl82957 Human PRO

10	750	100.0	390	8	ADN12256	Adn12256	Human	TSG
11	750	100.0	390	8	ADO43235	Ado43235	Human	TSG
12	750	100.0	390	8	ADO43233	Ado43233	Human	TSG
13	750	100.0	390	8	ADP82614	Adp82614	Human	tum
14	705	94.0	380	2	AAW19111	Aaw19111	Human	tum
15	693	92.4	391	6	AAE34884	Aae34884	Mouse	Tsg
16	693	92.4	391	7	ADB85228	Adb85228	Mouse	tum
17	648	86.4	381	2	AAW19110	Aaw19110	Mouse	tum
18	648	86.4	381	2	AAW93425	Aaw93425	Mouse	tsg
19	648	86.4	381	6	ABG73788	Abg73788	Murine	ts
20	648	86.4	381	7	ADC35178	Adc35178	Human	tsg
21	479	63.9	90	3	AAG01689	Aag01689	Human	sec
22	427	56.9	379	5	ABP43551	Abp43551	L-lactate	
23	427	56.9	379	8	ADH13697	Adh13697	Human	ENZ
24	363	48.4	341	4	AAB93473	Aab93473	Human	pro
25	363	48.4	433	7	ADM29340	Adm29340	Human	nov
26	346	46.1	146	3	AAB53717	Aab53717	Human	col
27	331	44.1	452	4	AAU23116	Aau23116	Novel	hum
28	328	43.7	73	8	ABO55495	Abo55495	Human	gen
29	276.5	36.9	398	3	AAG06370	Aag06370	Arabidops	
30	276.5	36.9	398	8	ADN73283	Adn73283	Thale	cre
31	276.5	36.9	412	3	AAG06369	Aag06369	Arabidops	
32	245.5	32.7	340	3	AAG06371	Aag06371	Arabidops	
33	239	31.9	331	4	ABB64607	Abb64607	Drosophil	
34	201.5	26.9	322	3	AAG13898	Aag13898	Arabidops	
35	107	14.3	307	5	ABP41729	Abp41729	Human	ova
36	106	14.1	123	4	ABG03740	Abg03740	Novel	hum
37	89.5	11.9	527	4	AAM80181	Aam80181	Human	pro
38	89.5	11.9	1648	3	AAB43174	Aab43174	Human	ORF
39	89.5	11.9	1867	4	AAB95564	Aab95564	Human	pro
40	89.5	11.9	4829	4	AAB97833	Aab97833	Human	apo
41	89	11.9	288	3	AAG13899	Aag13899	Arabidops	
42	88	11.7	18	8	ADN12257	Adn12257	Human	TSG
43	85.5	11.4	192	3	AAG04759	Aag04759	Arabidops	
44	85.5	11.4	254	7	ADH88640	Adh88640	Enterococ	
45	85.5	11.4	258	7	ADC94862	Adc94862	E. faeciu	



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 12.8861 Seconds  
(without alignments)  
1045.338 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_1\_140  
Perfect score: 750  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	299.5	39.9	404	2	H88650	protein C09G12.9 [
2	96.5	12.9	179	2	T34367	hypothetical prote
3	95.5	12.7	212	2	S74288	hypothetical prote
4	87.5	11.7	4845	2	T31067	BIR repeat contain
5	83.5	11.1	666	2	T40172	Glucose inhibited
6	82.5	11.0	940	2	AD1374	internalin protein
7	80	10.7	423	2	T15350	hypothetical prote
8	80	10.7	940	2	AB1744	internalin protein
9	79.5	10.6	800	2	T26683	hypothetical prote
10	79	10.5	1088	1	P1XRPR	inner layer protei
11	78.5	10.5	194	2	S57619	ubiquitin conjugat
12	78.5	10.5	1088	1	P1XRSR	inner layer protei
13	78.5	10.5	1088	2	S13558	VP1 protein - bovi

14	77	10.3	1088	2	S39261	VP1 protein - porc
15	76.5	10.2	144	2	G90107	ubiquitin-conjugat
16	76.5	10.2	458	2	T13819	NADH2 dehydrogenas
17	76	10.1	666	2	D42510	O1L protein - vacc
18	76	10.1	763	2	D83905	hypothetical prote
19	75.5	10.1	708	2	T47650	ABC transporter-li
20	74.5	9.9	147	2	D90126	ubiquitin-conjugat
21	74.5	9.9	754	2	AG1265	protein-export mem
22	74.5	9.9	1088	1	P1XRBR	inner layer protei
23	73.5	9.8	247	2	JU0393	karasurin - Mongol
24	73.5	9.8	247	2	JC5032	karasurin-B - Tric
25	73.5	9.8	289	1	RLTZT	rRNA N-glycosidase
26	73.5	9.8	289	2	JC5606	karasurin C - Tric
27	73.5	9.8	1738	2	S20614	conserved hypothet
28	73	9.7	296	2	F91145	probable methyltra
29	73	9.7	296	2	B85991	probable methyltra
30	73	9.7	296	2	H65118	hypothetical adeni
31	72.5	9.7	154	2	JC6163	ubiquitin-conjugat
32	72.5	9.7	269	2	F85063	hypothetical prote
33	72.5	9.7	803	2	S76106	hypothetical prote
34	72	9.6	218	2	B53516	ubiquitin-protein
35	72	9.6	475	1	S46941	translation initia
36	71.5	9.5	295	2	AC2357	DNA-methyltransfer
37	71.5	9.5	626	2	T08926	hypothetical prote
38	71	9.5	778	2	B71164	probable beta-gala
39	70.5	9.4	240	1	C69114	conserved hypothet
40	70.5	9.4	566	2	A59285	myosin-VIIa motor
41	70	9.3	702	2	S59428	probable membrane
42	70	9.3	888	1	GNLJHD	pol polyprotein -
43	69.5	9.3	154	2	T13578	ubiquitin-conjugat
44	69.5	9.3	230	2	T16479	hypothetical prote
45	69.5	9.3	238	2	AH0164	arginine transport

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 67.7067 Seconds  
(without alignments)  
1189.726 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_1\_140  
Perfect score: 750  
Sequence: 1 MAVSESQLKKMVSKYKYRDL.....QSDLLGLIQVMIVVFGDEPP 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	750	100.0	390	1	T101_HUMAN	Q99816	homo sapien
2	750	100.0	390	2	Q9BUM5	Q9bum5	homo sapien
3	693	92.4	391	1	T101_MOUSE	Q61187	mus musculu
4	693	92.4	391	2	Q6IRE4	Q6ire4	rattus norv
5	693	92.4	391	2	AAH70951	Aah70951	rattus no
6	693	92.4	392	2	Q9I8G8	Q9i8g8	chelonias my
7	684	91.2	391	2	Q7TSE5	Q7tse5	rattus norv
8	676	90.1	326	2	Q6DDX9	Q6ddx9	xenopus lae
9	673	89.7	394	2	Q6NUD5	Q6nud5	xenopus lae
10	673	89.7	394	2	AAH68660	Aah68660	xenopus l
11	670	89.3	395	2	Q6P2Z8	Q6p2z8	xenopus tro
12	670	89.3	395	2	AAH64236	Aah64236	xenopus t
13	650	86.7	390	2	Q6IQ70	Q6iq70	brachydanio
14	650	86.7	390	2	AAH71540	Aah71540	brachydan
15	522	69.6	114	2	Q7T2M2	Q7t2m2	ameiurus ne

16	454	60.5	249	2	Q8MQZ0	Q8mqz0 drosophila
17	454	60.5	408	2	Q9VVA7	Q9vva7 drosophila
18	428	57.1	402	2	Q7Q6B6	Q7q6b6 anopheles g
19	427	56.9	379	2	Q8IX04	Q8ix04 homo sapien
20	415	55.3	174	2	O08761	O08761 mus musculu
21	409.5	54.6	249	2	Q7TQD3	Q7tqd3 mus musculu
22	397	52.9	471	2	Q6DBY5	Q6dby5 brachydanio
23	363	48.4	177	2	Q96FF5	Q96ff5 homo sapien
24	363	48.4	341	2	Q9NUX7	Q9nux7 homo sapien
25	342	45.6	425	2	O76258	O76258 caenorhabdi
26	333	44.4	357	2	Q6P2F0	Q6p2f0 homo sapien
27	333	44.4	357	2	AAH64566	Aah64566 homo sapi
28	280	37.3	111	2	Q8BU96	Q8bu96 mus musculu
29	276.5	36.9	398	2	Q9LHG8	Q9lhg8 arabidopsis
30	252.5	33.7	368	2	Q9FFY6	Q9fffy6 arabidopsis
31	252	33.6	580	2	Q7S4R9	Q7s4r9 neurospora
32	212	28.3	402	2	Q6ESB7	Q6esb7 oryza sativ
33	152.5	20.3	496	2	Q6BID5	Q6bid5 debaryomyce
34	150	20.0	385	1	ST22_YEAST	P25604 saccharomyc
35	150	20.0	468	2	Q6FS29	Q6fs29 candida gla
36	120.5	16.1	376	2	P78998	P78998 saccharomyc
37	109.5	14.6	445	2	Q75EU1	Q75eu1 ashbya goss
38	109.5	14.6	445	2	AAS50360	Aas50360 ashbya go
39	96.5	12.9	179	2	Q22577	Q22577 caenorhabdi
40	93	12.4	378	2	Q873M7	Q873m7 yarrowia li
41	93	12.4	378	2	Q6C148	Q6c148 yarrowia li
42	89.5	11.9	1867	2	Q9H8B7	Q9h8b7 homo sapien
43	89.5	11.9	4829	1	BIR6_HUMAN	Q9nr09 homo sapien
44	88.5	11.8	694	2	Q759K3	Q759k3 ashbya goss
45	88.5	11.8	694	2	AAS52194	Aas52194 ashbya go

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 49.1794 Seconds  
(without alignments)  
809.667 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_140\_250  
Perfect score: 615  
Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	615	100.0	307	5	ABP41729	Abp41729 Human ova
2	615	100.0	380	2	AAW19111	Aaw19111 Human tum
3	615	100.0	390	2	AAW93424	Aaw93424 Human NHT
4	615	100.0	390	5	ABP52191	Abp52191 Human tum
5	615	100.0	390	6	AAE34885	Aae34885 Human Tsg
6	615	100.0	390	6	ABG73787	Abg73787 Human tum
7	615	100.0	390	7	ADC35176	Adc35176 Novel hum
8	615	100.0	390	8	ADF91425	Adf91425 TSG101 #S
9	615	100.0	390	8	ADL82957	Adl82957 Human PRO

10	615	100.0	390	8	ADN12256	Adn12256	Human	TSG
11	615	100.0	390	8	ADO43235	Ado43235	Human	TSG
12	615	100.0	390	8	ADO43233	Ado43233	Human	TSG
13	615	100.0	390	8	ADP82614	Adp82614	Human	tum
14	570.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum
15	570.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg
16	570.5	92.8	381	6	ABG73788	Abg73788	Murine	ts
17	570.5	92.8	381	7	ADC35178	Adc35178	Human	tsg
18	570.5	92.8	391	6	AAE34884	Aae34884	Mouse	Tsg
19	570.5	92.8	391	7	ADB85228	Adb85228	Mouse	tum
20	419	68.1	237	4	AAE09328	Aae09328	Human	int
21	209	34.0	331	4	ABB64607	Abb64607	Drosophil	
22	144	23.4	218	4	ABG18833	Abg18833	Novel	hum
23	140.5	22.8	148	3	AAAY86515	Aay86515	Human	gen
24	140.5	22.8	148	5	ABB97431	Abb97431	Novel	hum
25	140.5	22.8	148	6	ABO53679	Abo53679	Novel	hum
26	140.5	22.8	176	4	AAG75132	Aag75132	Human	col
27	138.5	22.5	485	3	AAB57086	Aab57086	Human	pro
28	137.5	22.4	466	2	AAR07084	Aar07084	Recombina	
29	137.5	22.4	466	6	ABO07215	Abo07215	Human	p53
30	137.5	22.4	466	7	ADD47589	Add47589	Human	Pro
31	137.5	22.4	466	7	ADI15879	Adi15879	Human	PP
32	137.5	22.4	466	7	ADJ68571	Adj68571	Human	hea
33	136.5	22.2	258	3	AAB44500	Aab44500	Plant	vir
34	134.5	21.9	244	3	AAG40015	Aag40015	Arabidops	
35	134.5	21.9	245	3	AAG38059	Aag38059	Arabidops	
36	134.5	21.9	245	3	AAG05889	Aag05889	Arabidops	
37	134.5	21.9	247	3	AAG38058	Aag38058	Arabidops	
38	134.5	21.9	247	3	AAG05888	Aag05888	Arabidops	
39	134.5	21.9	263	3	AAG38057	Aag38057	Arabidops	
40	134.5	21.9	274	3	AAG05887	Aag05887	Arabidops	
41	130	21.1	172	4	ABG18832	Abg18832	Novel	hum
42	127.5	20.7	262	8	ADN17284	Adn17284	Chicken	g
43	127.5	20.7	505	2	AAAY07117	Aay07117	Lung	canc
44	127.5	20.7	505	6	ABO07216	Abo07216	Human	p53
45	127.5	20.7	505	7	ADJ68733	Adj68733	Human	hea

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:40:45 ; Search time 10.2168 Seconds  
 (without alignments)  
 1045.338 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_140\_250  
 Perfect score: 615  
 Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	186	30.2	404	2	H88650	protein C09G12.9 [
2	145.5	23.7	169	2	T34520	hypothetical prote
3	131.5	21.4	488	1	LUHU7	annexin VII, long
4	127.5	20.7	198	2	D70509	hypothetical prote
5	127.5	20.7	505	2	A53152	annexin XI - human
6	123.5	20.1	503	1	LURB11	annexin XI - rabbi
7	122.5	19.9	279	2	T05421	hypothetical prote
8	122.5	19.9	463	2	S29170	annexin VII - mous
9	121.5	19.8	1880	2	T18531	tractin - medicina
10	119.5	19.4	671	2	T36037	probable export as
11	118	19.2	176	2	A86441	hypothetical prote
12	116.5	18.9	316	2	T20497	hypothetical prote
13	115.5	18.8	177	2	S65780	glycine/proline-ri

14	115.5	18.8	491	2	S14182	DNA-directed RNA p
15	115.5	18.8	650	2	S14181	DNA-directed RNA p
16	115	18.7	240	2	D70894	probable pra prote
17	115	18.7	564	2	H70804	hypothetical prote
18	113	18.4	481	2	F86208	protein F22G5.30 [
19	112	18.2	1357	2	T29265	hypothetical prote
20	112	18.2	1691	1	S22917	collagen alpha 5(I
21	111.5	18.1	1049	1	CGBO7S	collagen alpha 1(I
22	111	18.0	214	2	T10737	extensin-like cell
23	111	18.0	214	2	T09854	proline-rich cell
24	111	18.0	2715	2	T13049	eyelid - fruit fly
25	110.5	18.0	388	2	JC5437	spliceosome-associ
26	110.5	18.0	451	2	B70792	hypothetical prote
27	110.5	18.0	977	2	S14183	DNA-directed RNA p
28	110	17.9	324	2	G86222	hypothetical prote
29	110	17.9	324	2	T51602	shock protein SRC2
30	110	17.9	503	1	LUBO11	annexin XI form A
31	110	17.9	505	1	S23447	annexin XI form B
32	109.5	17.8	1008	2	T04462	hypothetical prote
33	109.5	17.8	1069	2	D85383	hypothetical prote
34	108.5	17.6	428	2	T24769	hypothetical prote
35	108	17.6	467	2	A27677	DNA-directed RNA p
36	108	17.6	1932	1	A28490	DNA-directed RNA p
37	108	17.6	1970	1	S21054	DNA-directed RNA p
38	108	17.6	1970	2	I38186	RNA polymerase II
39	107.5	17.5	179	2	A85217	hypothetical prote
40	107.5	17.5	277	2	T04441	hypothetical prote
41	107.5	17.5	569	2	S42886	collagen - silkwor
42	107.5	17.5	886	2	I50694	collagen alpha 1(I
43	107	17.4	199	2	S14981	extensin class I (
44	107	17.4	299	2	T29956	hypothetical prote
45	106.5	17.3	294	2	A49688	lactose-binding le



OM protein - protein search, using sw model

Run on: December 20, 2004, 15:26:03 ; Search time 53.6817 Seconds  
(without alignments)  
1189.726 Million cell updates/sec

Title: US-10-053-975A-1\_COPY\_140\_250  
Perfect score: 615  
Sequence: 1 PVFSRPISASYPPYQATGPP.....ISAVSDKLRWRMKEEMDRAQ 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	615	100.0	390	1	T101_HUMAN	Q99816	homo sapien
2	615	100.0	390	2	Q9BUM5	Q9bum5	homo sapien
3	570.5	92.8	391	1	T101_MOUSE	Q61187	mus musculu
4	552.5	89.8	391	2	Q6IRE4	Q6ire4	rattus norv
5	552.5	89.8	391	2	AAH70951	Aah70951	rattus no
6	545.5	88.7	391	2	Q7TSE5	Q7tse5	rattus norv
7	529	86.0	392	2	Q9I8G8	Q9i8g8	chelonias my
8	405.5	65.9	390	2	Q6IQ70	Q6iq70	brachydanio
9	405.5	65.9	390	2	AAH71540	Aah71540	brachydan
10	383.5	62.4	395	2	Q6P2Z8	Q6p2z8	xenopus tro
11	383.5	62.4	395	2	AAH64236	Aah64236	xenopus t
12	383	62.3	394	2	Q6NUD5	Q6nud5	xenopus lae
13	383	62.3	394	2	AAH68660	Aah68660	xenopus l
14	209	34.0	408	2	Q9VVA7	Q9vva7	drosophila
15	194	31.5	425	2	O76258	O76258	caenorhabdi

16	166.5	27.1	402	2	Q7Q6B6	Q7q6b6 anopheles g
17	152	24.7	249	2	Q8MQZ0	Q8mqz0 drosophila
18	145.5	23.7	148	2	Q9NTQ8	Q9ntq8 homo sapien
19	145	23.6	485	2	Q804G3	Q804g3 brachydanio
20	145	23.6	485	2	AAH68366	Aah68366 brachydan
21	140.5	22.8	148	2	Q6NXQ6	Q6nxq6 homo sapien
22	140.5	22.8	148	2	Q9NZ81	Q9nz81 homo sapien
23	140.5	22.8	148	2	AAH66943	Aah66943 homo sapi
24	137.5	22.4	466	1	ANX7_HUMAN	P20073 homo sapien
25	137.5	22.4	466	2	BAB93492	Bab93492 homo sapi
26	137.5	22.4	466	2	AAP35851	Aap35851 homo sapi
27	137.5	22.4	466	2	CAG28614	Cag28614 homo sapi
28	136	22.1	483	2	Q7T391	Q7t391 brachydanio
29	134.5	21.9	247	2	Q945K9	Q945k9 arabidopsis
30	134.5	21.9	247	2	AAT41866	Aat41866 arabidops
31	130	21.1	664	2	Q6CDQ5	Q6cdq5 yarrowia li
32	129.5	21.1	332	2	Q8QGD9	Q8qgd9 gallus gall
33	128.5	20.9	345	2	Q9ESF4	Q9esf4 mus musculu
34	127.5	20.7	198	2	O86316	O86316 mycobacteri
35	127.5	20.7	201	2	Q7D8K1	Q7d8k1 mycobacteri
36	127.5	20.7	262	2	Q90713	Q90713 gallus gall
37	127.5	20.7	471	2	Q9LD31	Q9ld31 crypthecodi
38	127.5	20.7	505	1	ANXB_HUMAN	P50995 homo sapien
39	127.5	20.7	505	2	CAG29319	Cag29319 homo sapi
40	126.5	20.6	137	2	Q9CQJ5	Q9cqj5 m mus muscu
41	126.5	20.6	171	2	Q7SA74	Q7sa74 neurospora
42	126	20.5	192	2	Q9VKM5	Q9vkm5 drosophila
43	126	20.5	343	2	Q8IVW7	Q8ivw7 homo sapien
44	126	20.5	371	2	Q7Z429	Q7z429 homo sapien
45	126	20.5	868	1	PD6I_HUMAN	Q8wum4 homo sapien

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:24:58 ; Search time 172.793 Seconds  
 (without alignments)  
 809.667 Million cell updates/sec

Title: US-10-053-975A-1  
 Perfect score: 2047  
 Sequence: 1 MAVSESQLKKMVSQKYYRDL.....FQLRALMQKARKTAGLSPLY 390

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
 1: \_geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2047	100.0	390	2 AAW93424	Aaw93424 Human NHT
2	2047	100.0	390	5 ABP52191	Abp52191 Human tum
3	2047	100.0	390	6 ABG73787	Abg73787 Human tum

Untitled									
4	2047	100.0	390	7	ADC35176	Adc35176	Novel	hum	
5	2047	100.0	390	8	AdF91425	Adf91425	TSG101	#S	
6	2047	100.0	390	8	AdL82957	Adl82957	Human	PRO	
7	2047	100.0	390	8	ADN12256	Adn12256	Human	TSG	
8	2047	100.0	390	8	ADO43235	Ado43235	Human	TSG	
9	2047	100.0	390	8	ADO43233	Ado43233	Human	TSG	
10	2047	100.0	390	8	ADP82614	Adp82614	Human	tum	
11	2042	99.8	390	6	AAE34885	Aae34885	Human	Tsg	
12	2002	97.8	380	2	AAW19111	Aaw19111	Human	tum	
13	1945.5	95.0	391	6	AAE34884	Aae34884	Mouse	Tsg	
14	1945.5	95.0	391	7	ADB85228	Adb85228	Mouse	tum	
15	1900.5	92.8	381	2	AAW19110	Aaw19110	Mouse	tum	
16	1900.5	92.8	381	2	AAW93425	Aaw93425	Mouse	tsg	
17	1900.5	92.8	381	6	ABG73788	Abg73788	Murine	ts	
18	1900.5	92.8	381	7	ADC35178	Adc35178	Human	tsg	
19	1404	68.6	307	5	ABP41729	Abp41729	Human	ova	
20	1162	56.8	237	4	AAE09328	Aae09328	Human	int	
21	809.5	39.5	331	4	ABB64607	Abb64607	Drosophi1		
22	776	37.9	145	8	ADF91424	Adf91424	TSG101UEV		
23	479	23.4	90	3	AAG01689	Aag01689	Human	sec	
24	455	22.2	398	3	AAG06370	Aag06370	Arabidops		
25	455	22.2	398	8	ADN73283	Adn73283	Thale cre		
26	455	22.2	412	3	AAG06369	Aag06369	Arabidops		
27	435	21.3	379	5	ABP43551	Abp43551	L-lactate		
28	435	21.3	379	8	ADH13697	Adh13697	Human	ENZ	
29	424	20.7	340	3	AAG06371	Aag06371	Arabidops		
30	390	19.1	87	8	ABO55273	Abo55273	Human	gen	
31	380	18.6	322	3	AAg13898	Aag13898	Arabidops		
32	371	18.1	341	4	AAB93473	Aab93473	Human	pro	
33	371	18.1	433	7	ADM29340	Adm29340	Human	nov	
34	346	16.9	146	3	AAAB53717	Aab53717	Human	col	
35	339	16.6	452	4	AAU23116	Aau23116	Novel	hum	
36	328	16.0	73	8	ABO55495	Abo55495	Human	gen	
37	267.5	13.1	288	3	AAg13899	Aag13899	Arabidops		
38	161.5	7.9	168	3	AAg13900	Aag13900	Arabidops		
39	161	7.9	485	3	AAAB57086	Aab57086	Human	pro	
40	160	7.8	466	6	ABO07215	Abo07215	Human	p53	
41	160	7.8	466	7	ADD47589	Add47589	Human	Pro	
42	160	7.8	466	7	ADL15879	Adl15879	Human	PP	
43	160	7.8	466	7	ADJ68571	Adj68571	Human	hea	
44	153	7.5	218	4	ABG18833	Abg18833	Novel	hum	
45	151	7.4	466	2	AAr07084	Aar07084	Recombina		

AAW93424  
 ID AAW93424 standard; protein; 390 AA.  
 XX  
 AC AAW93424;  
 XX  
 DT 11-JUN-1999 (first entry)

Query Match	100.0%;	Score 2047;	DB 2;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 6.7e-149;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
OY      1 MAVSSQLKMWSKYYRDLTVBETVNVITLYKDLPVLDSIVENDGSSRELMLNTGTIP   60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dp      1 MAVSESQLKMWSKYYRDLTVBETVNVITLYKDLPVLDSIYFENDGSSREIMNLGTIP   60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      61 VPRGNVTYNIPICIMLLDTYPYNPBICFVKPTTSMTIKTGHVDANGKIYPLLHEWKHP 120
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Untitled

Db 61 VPYRGNTYNIPICIWLLDTPYNPNPICFVKPTSSMTIKTGKHDVANGKIYLPYLHEWKHP 120

QY 121 QSDLLGLIQVMIVFEGDEPVPFSPRISASYPYQATGPNTSYMPGMPGISPYPSSGYPP 180  
 |||||  
 Db 121 QSDLLGLIQVMIVFEGDEPVPFSPRISASYPYQATGPNTSYMPGMPGISPYPSSGYPP 180

QY 181 NPSGYPGCPYPGPGYPATSSQYPSQPPVTIVGPSRDGTISEDTIRASLISAVSDKLRW 240  
 |||||  
 Db 181 NPSGYPGCPYPGPGYPATSSQYPSQPPVTIVGPSRDGTISEDTIRASLISAVSDKLRW 240

QY 241 RMKEEMDRAQAEINALKRTEEDLKKGHQKLEEMVTRLDQEVAEVDKNIELKKKDEELSS 300  
 |||||  
 Db 241 RMKEEMDRAQAEINALKRTEEDLKKGHQKLEEMVTRLDQEVAEVDKNIELKKKDEELSS 300

QY 301 ALEKMEÑOSENNDIDEVITPTAPLYKQILNLVYAEENAIEDTIFYLGEALRRGVIDLDFVL 360  
 |||||  
 Db 301 ALEKMEÑOSENNDIDEVITPTAPLYKQILNLVYAEENAIEDTIFYLGEALRRGVIDLDFVL 360

QY 361 KHVRLLSRKQFQLRALMOKARKTAGLSLDY 390  
 |||||  
 Db 361 KHVRLLSRKQFQLRALMOKARKTAGLSLDY 390

RESULT 2

AAE09328  
 ID AAE09328 standard; protein; 237 AA.  
 XX  
 AC AAE09328;  
 XX  
 DT 19-NOV-2001 (first entry)  
 XX  
 DE Human intracellular regulatory molecule, tsq101.  
 XX  
 KW Human; intracellular regulator; cell division; proliferation; therapy;  
 KW cancer; infection; wound; developmental abnormality; metabolic problem;  
 KW cytostatic; antibacterial; vulnery; transcription factor; tsq101.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6274312-B1.  
 XX  
 PD 14-AUG-2001.  
 XX  
 PF 10-DEC-1997; 97US-00999774.  
 XX  
 PR 11-DEC-1996; 96US-0032818P.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gish KC, Seghezzi W, Shanahan F, Lees EM, McClanahan TK;  
 XX